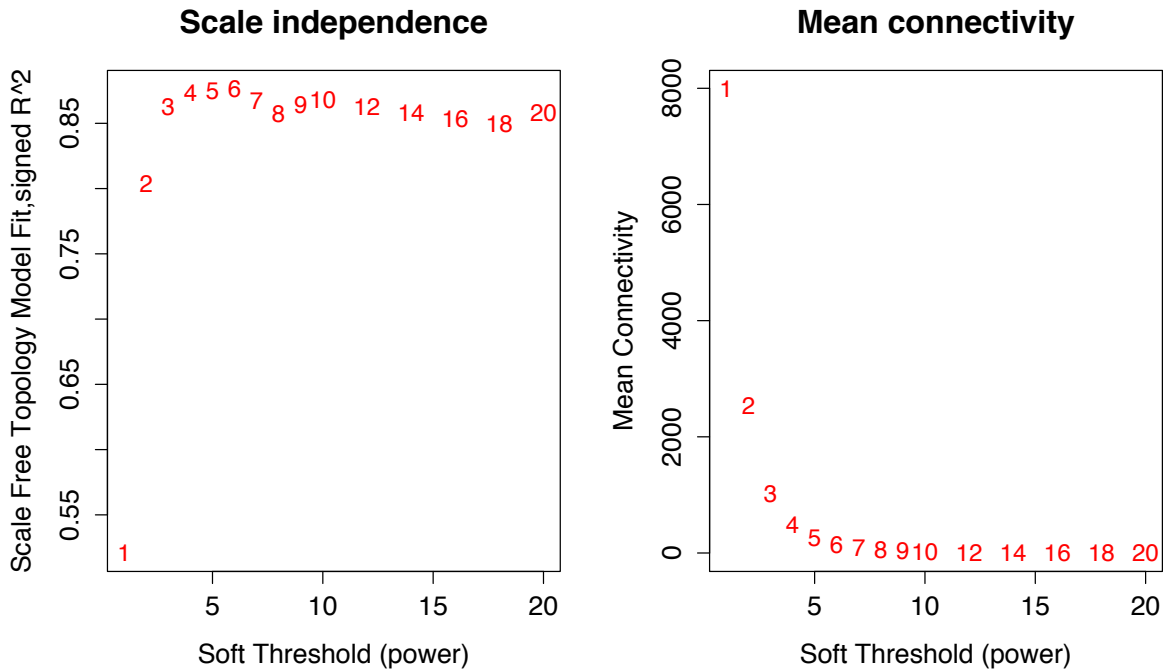


SUPPLEMENTAL RESULTS

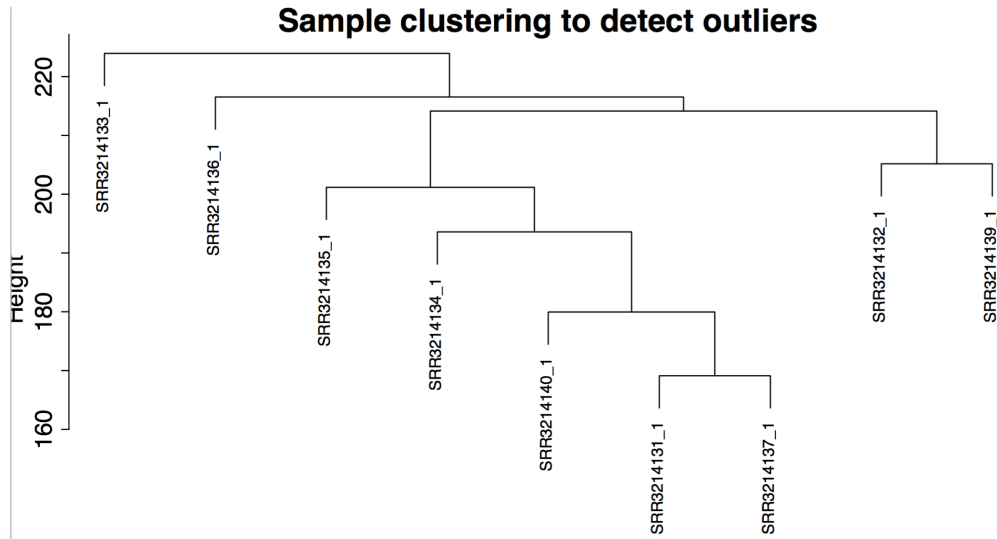
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The following figures and tables support the main text.



5

6 **Figure S1.** Soft threshold power selection in the female Brook Charr network after outliers were removed. Both
7 (A) scale independence and (B) mean connectivity are used to determine the best soft threshold power. Scale free
8 topology was chosen as $\beta_1=6$, which also is the default for WGCNA.

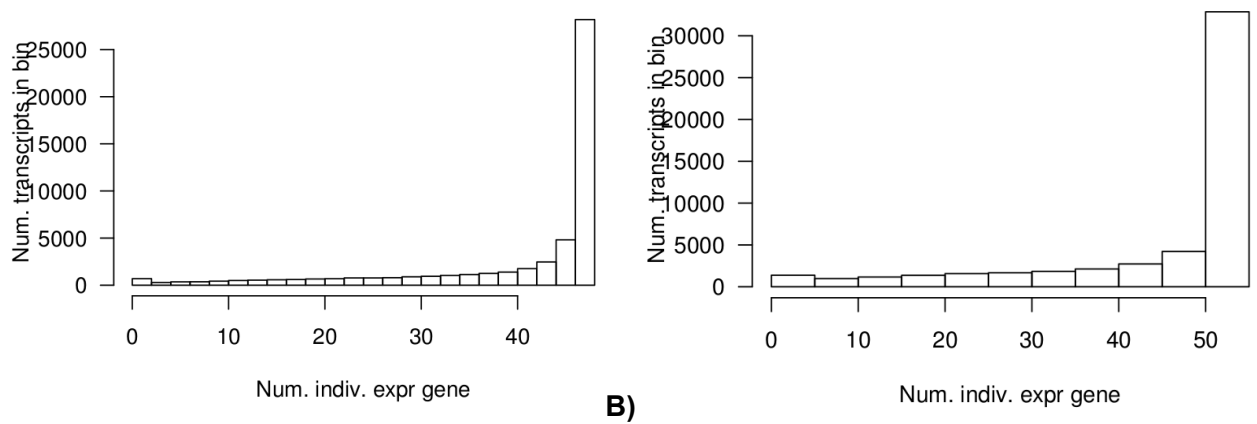


10

11 **Figure S2.** Nine individual male Arctic Charr samples clustered by gene expression similarity. Only the samples
 12 from the control condition (8 °C) were used to avoid large experimental effects on the data and to make parallel
 13 with the Brook Charr data.

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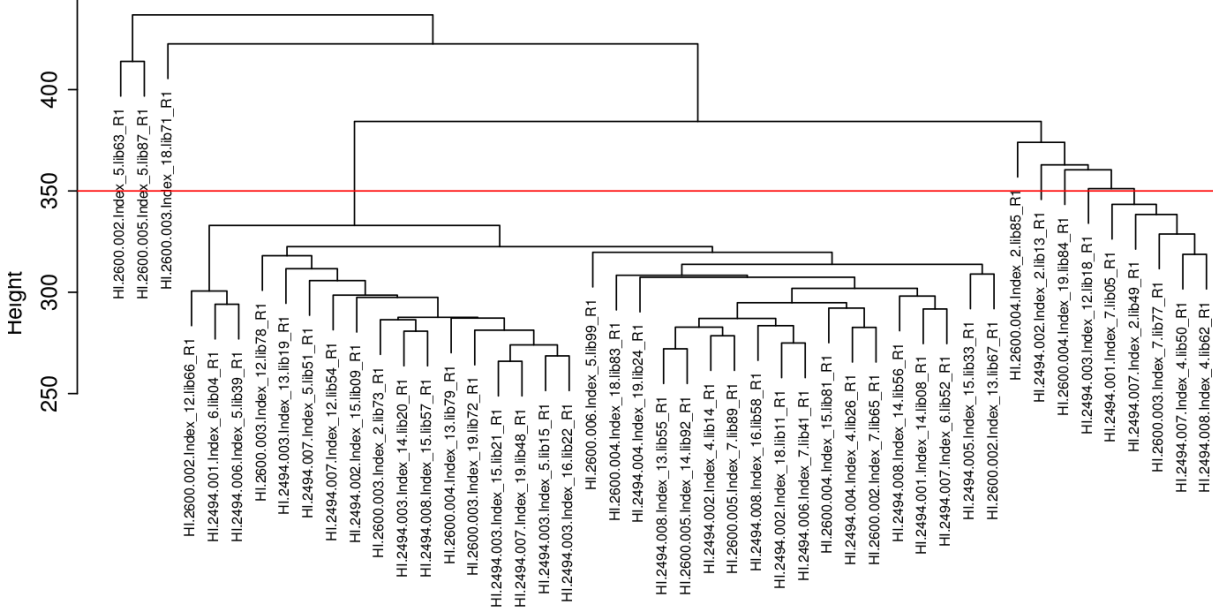
18 **Figure S3.** The number of transcripts expressed in the number of individuals in the Brook Charr (A) females and
 19 (B) males. This indicates that most genes, when found to be expressed at all, were expressed in most individuals.
 20 Within a sex, very few genes showed expression specific to a small number of samples.

20

21

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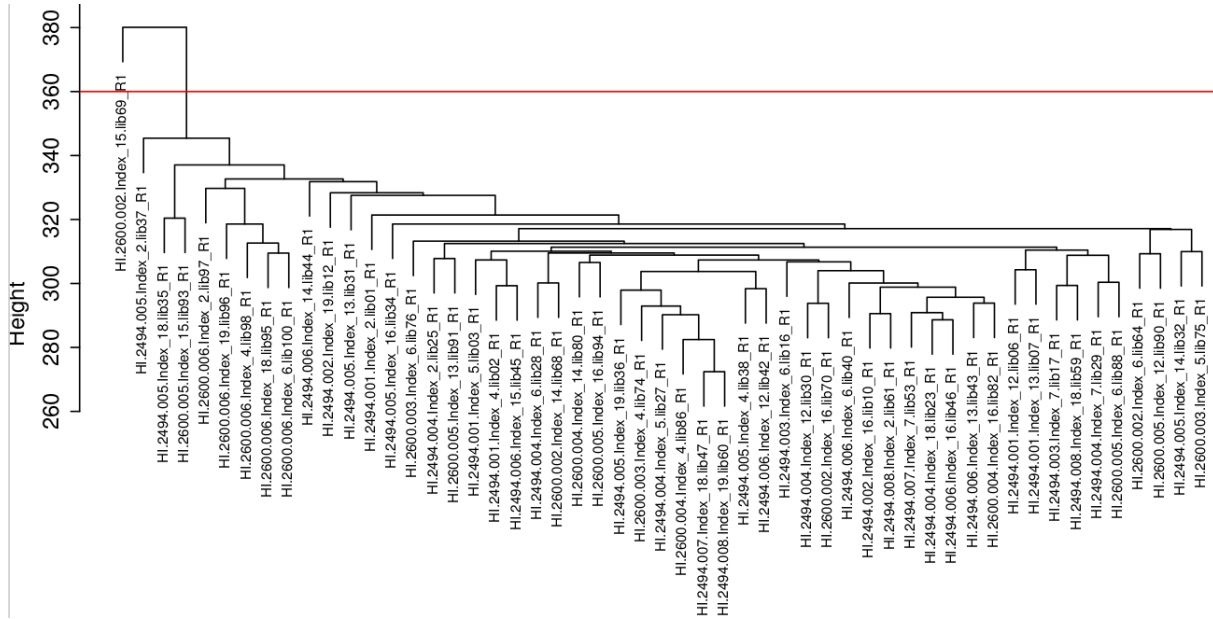
A)



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B)



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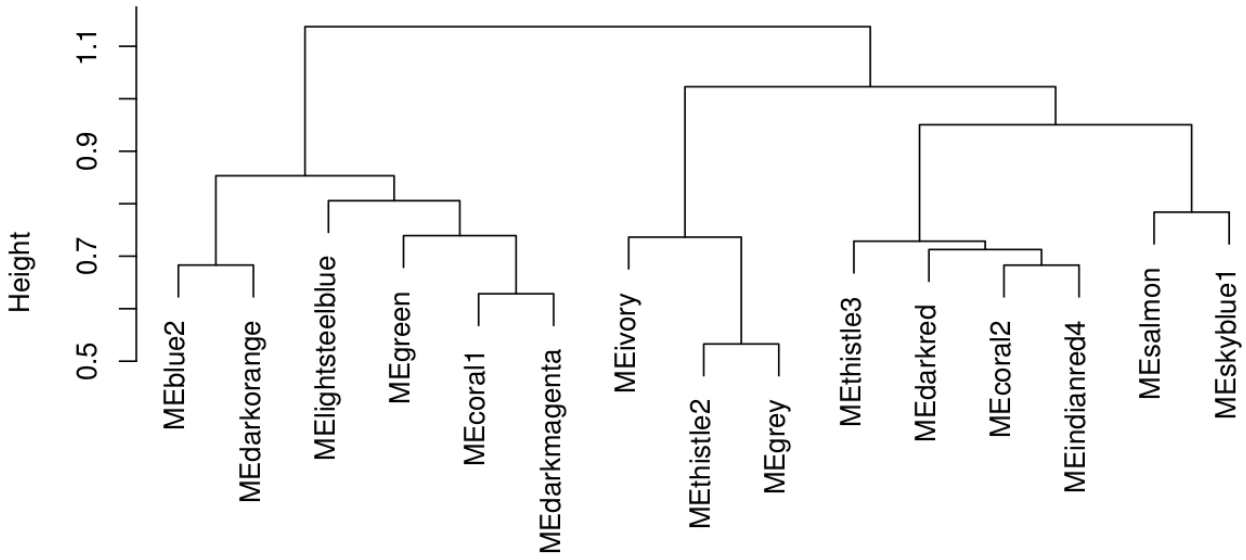
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Figure S4. Clustering of samples by transcriptome similarity within (A) females and (B) males. Outliers were removed by discarding samples that did not group with the rest of the samples according to the cut height shown by the red horizontal line. Selection of cut height was determined by observing the clustering of samples with phenotypes and removing groups that did not fit with the rest of the samples, which included one extreme outlier male (also see Figure 1) and a subset of females with large liver weight. See Methods for further discussion on justification for outlier removal.

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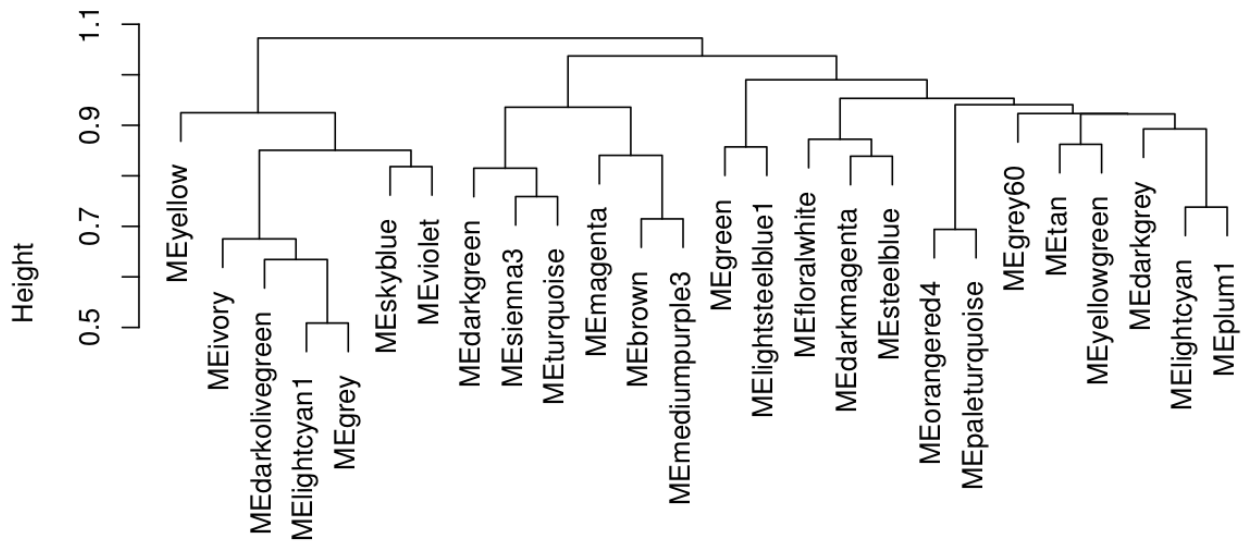
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35 **A)**



36

37 **B)**



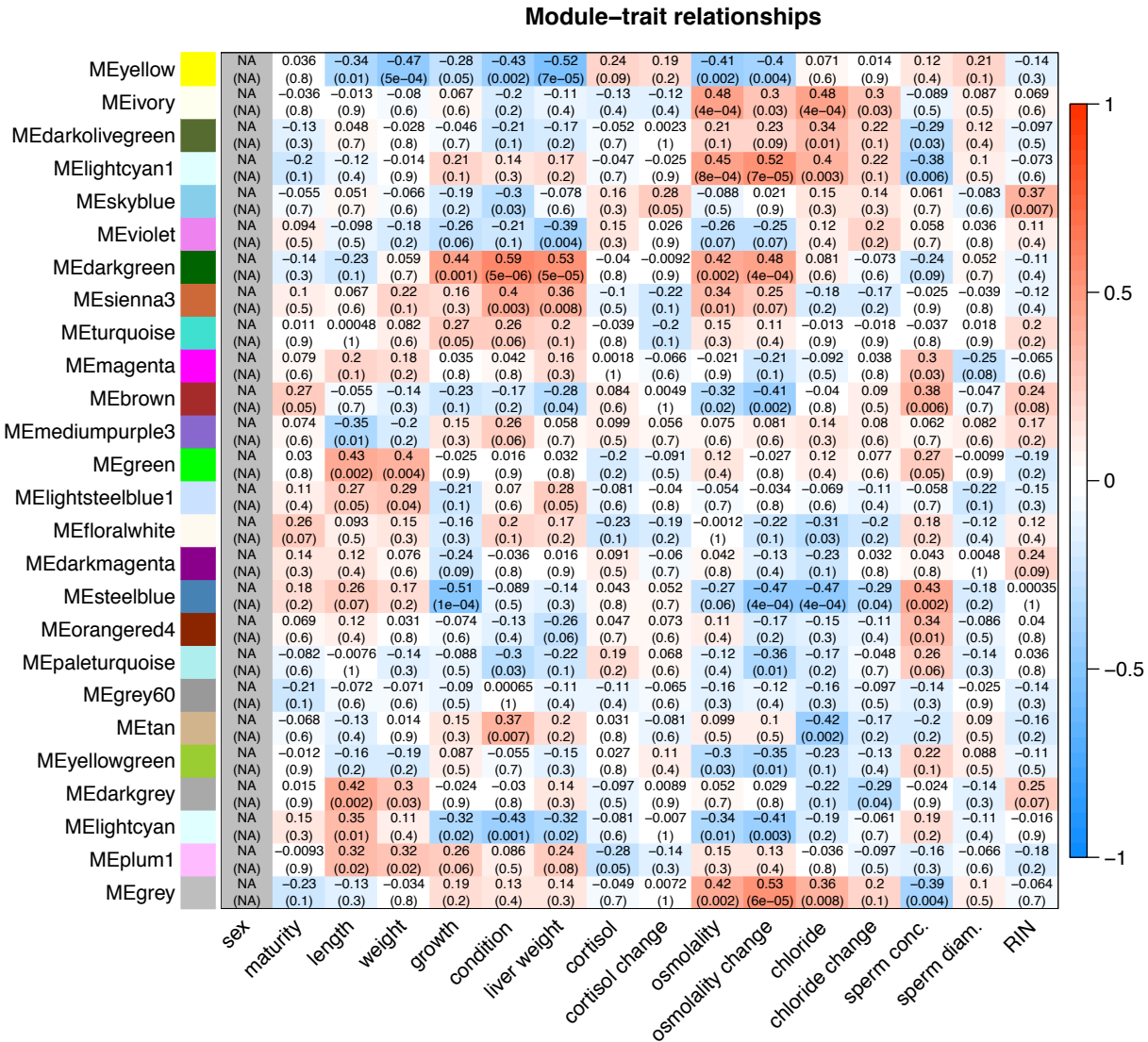
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39 **Figure S5.** Merged modules clustered by eigengene similarity in (A) female and (B) male Brook Charr.

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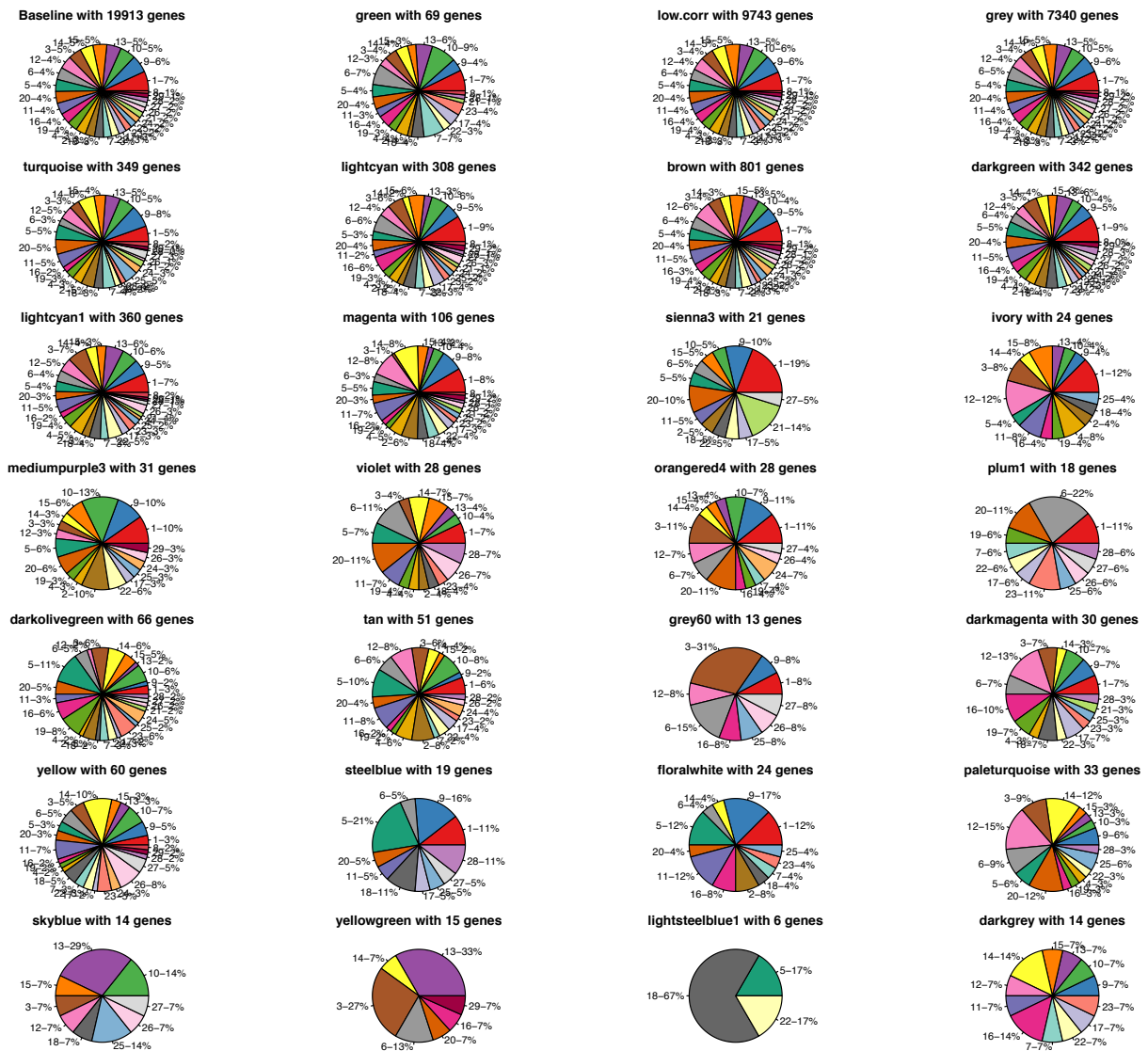
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44 **Figure S6.** Module-trait relationships for Brook Charr males, including correlation r-value and p-values. The
 45 boldness of color indicates the strength of the relationship. Module-trait correlations are also shown in Table 1
 46 with more general grouping of traits alongside other metrics such as module size and enriched Gene Ontology
 47 categories. Female module-trait relationships are shown in Figure 3.



55

56 **Figure S8.** Chromosome overrepresentation evaluated within the male clusters. The proportion of transcripts per
 57 chromosome is shown for the baseline (all expressed unique genes), and each male module. The name of the
 58 module and the number of genes within the module are shown above each chart. Significant overrepresented
 59 chromosomes and base pair location on chromosome positions are shown in Figure 8.

60

61 **Table S1.** Overrepresented chromosomes for individual female modules ($p \leq 0.05$) shown alongside the number
62 of genes within the chromosome in the module and the number of other genes in the module not in the
63 chromosome. Note: low.corr is comprised of the genes that are not within the most connected 25,000 genes put
64 into the network.

Chromosome RefSeq Accession	Chromosome Name	Module	P-value	Number of genes in chromosome in module	Number of genes not in chromosome in module
NC_027319.1	chr20	salmon	0.005	15	154
NC_027325.1	chr26	green	0.006	10	198
NC_027305.1	chr6	low.corr	0.009	383	9506
NC_027306.1	chr7	salmon	0.016	0	169
NC_027308.1	chr9	low.corr	0.018	645	9244
NC_027327.1	chr28	thistle3	0.026	5	92
NC_027320.1	chr21	low.corr	0.034	230	9659
NC_027328.1	chr29	coral2	0.034	4	80
NC_027316.1	chr17	darkorange	0.034	15	317
NC_027308.1	chr9	salmon	0.036	4	165
NC_027302.1	chr3	skyblue1	0.036	5	36
NC_027304.1	chr5	green	0.037	15	193
NC_027305.1	chr6	darkorange	0.038	22	310
NC_027310.1	chr11	indianred4	0.040	30	488
NC_027325.1	chr26	skyblue1	0.041	3	38
NC_027313.1	chr14	green	0.042	16	192
NC_027312.1	chr13	lightsteelblue	0.045	2	5
NC_027320.1	chr21	darkred	0.045	71	4088
NC_027305.1	chr6	darkred	0.047	200	3959
NC_027327.1	chr28	blue2	0.047	21	763
NC_027308.1	chr9	darkred	0.049	227	3932

65

66 **Table S2.** Overrepresented chromosomes for individual male modules ($p \leq 0.05$) shown alongside the number of
67 genes within the chromosome in the module and the number of other genes in the module not in the chromosome.
68 Note: low.corr is comprised of the genes that are not within the most connected 25,000 genes put into the network.

Chromosome RefSeq Accession	Chromosome Name	Module	P-value	Number of genes in chromosome in module	Number of genes not in chromosome in module
NC_027317.1	chr18	lightsteelblue1	1.42E-05	4	2
NC_027312.1	chr13	yellowgreen	0.001	5	10
NC_027316.1	chr17	turquoise	0.002	1	348
NC_027302.1	chr3	grey60	0.002	4	9
NC_027305.1	chr6	low.corr	0.004	372	9371
NC_027302.1	chr3	yellowgreen	0.004	4	11
NC_027312.1	chr13	skyblue	0.004	4	10
NC_027324.1	chr25	turquoise	0.005	16	333
NC_027325.1	chr26	yellow	0.005	5	55
NC_027305.1	chr6	plum1	0.006	4	14
NC_027304.1	chr5	steelblue	0.007	4	15
NC_027305.1	chr6	grey	0.009	348	6992
NC_027320.1	chr21	sienna3	0.009	3	18
NC_027307.1	chr8	low.corr	0.012	68	9675
NC_027321.1	chr22	lightcyan1	0.013	18	342
NC_027311.1	chr12	paleturquoise	0.015	5	28
NC_027304.1	chr5	darkolivegreen	0.021	7	59
NC_027316.1	chr17	low.corr	0.026	277	9466
NC_027311.1	chr12	brown	0.029	49	752
NC_027327.1	chr28	turquoise	0.034	1	348
NC_027324.1	chr25	skyblue	0.037	2	12
NC_027327.1	chr28	steelblue	0.041	2	17
NC_027306.1	chr7	green	0.043	5	64
NC_027311.1	chr12	darkmagenta	0.044	4	26
NC_027314.1	chr15	low.corr	0.045	506	9237
NC_027319.1	chr20	paleturquoise	0.046	4	29
NC_027312.1	chr13	lightcyan	0.048	8	300
NC_027300.1	chr1	sienna3	0.051	4	17

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